





AF039235 AF039235 1866 bp mRNA linear EST 13-MAR-1998  
 LOCUS AF039235 Human (J. Swensen) Homo sapiens cDNA clone 91-13, mRNA  
 DEFINITION sequence.  
 ACCESSION AF039235  
 VERSION AF039235.1 GI:2773139  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1866)  
 AUTHORS Mili,Y., Swensen,J., Stattuck-Elidens,D., Futreal,P.A., Harsman,K.,  
 Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M. and Ding,W.  
 TITLE A strong candidate for the breast and ovarian cancer susceptibility  
 gene BRCA1  
 JOURNAL Science 266 (5182), 66-71 (1994)  
 MEDLINE 95025896  
 COMMENT Contact: Jeff Swensen  
 Medical Informatics  
 University of Utah  
 391 Chipeta Way, Suite D-2, Salt Lake City, UT 84108, USA  
 Email: jeffsw@epi.sun5.med.utah.edu  
 region between D17S1321 and D17S855.  
 FEATURES  
 Source Location/Qualifiers  
 1. 1866  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="17q21"  
 /clone="91-13"  
 /clone\_lib="Human (J. Swensen)"  
 /note="Organ: Hip; Vector: pBluescript; Site: 1; EcoRI;  
 Library constructed by Dr. Marian Young and Dr. Pamela  
 Gehron Robey (NIDCR)"  
 BASE COUNT 466 a 423 c 568 g 408 t 1 others  
 ORIGIN  
 Query Match 77.3%; Score 432.2; DB 9; Length 1866;  
 Best Local Similarity 99.3%; Pred. No. 4e-117;  
 Matches 434; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 4  
 LOCUS AL520188 935 bp mRNA linear EST 13-FEB-2001  
 DEFINITION AL520188 LTI\_NFL004\_NBC2 Homo sapiens cDNA clone CS0DB005YN06 5  
 prime, mRNA sequence.  
 ACCESSION AL520188  
 VERSION AL520188.1 GI:12783681  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 935)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
 FEATURES  
 Source Location/Qualifiers  
 1. 935  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CS0DB005YN06"  
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 /sex="male"  
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 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed  
 by Life Technologies. Contact : Feng Liang Life  
 Technologies, a division of Invitrogen 9800 Medical Center  
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610  
 8371 Email : fliang@lifestech.com URL :  
 http://fulllength.invitrogen.com"  
 BASE COUNT 231 a 206 c 287 g 208 t 3 others  
 ORIGIN  
 Query Match 76.3%; Score 426.4; DB 9; Length 935;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-115;  
 Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 AACATATGACGACTTTTGAAGAAGTGCAGACACCAAGAGACCTCCACCTGCATGATG 420  
QY 430 ATTGGAT 437  
Db 421 ATTGGAT 428

RESULT 5  
AM245514  
LOCUS 577 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2823004.Sprime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2823004 5',  
mRNA sequence.  
ACCESSION AM245514  
VERSION AM245514.1 GI:6588507  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 577)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2823004.3prime  
Contact: Robert Strausberg, Ph.D.  
Email: rgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DPF cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LINP) DNA Sequencing by: Berkeley MGC sequencing  
project clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LINP at:  
www.bio.lnlnl.gov/dbnp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T identification: patchmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu  
plate: LHCMI0 row: 0 column: 5  
High quality sequence stop: 487.  
Location/Qualifiers  
1..577  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone IMAGE:2823004"  
/clone\_1lb="NIH\_MGC\_7"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAC(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 129 a 133 c 179 g 136 t  
ORIGIN  
Query Match 76.1%; Score 425.2; DB 10; Length 577;  
Best Local Similarity 99.3%; Pred. No. 2.8e-115;  
Matches 427; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GGCACGGCAGCAGCCCGGACCTTGTTGATGACAGAGCCCATGTATGTTCATGAGTT 67  
Db 103 GGGAAAGCAGCAGCCCGGACCTTGTTGATGACAGAGCCCATGTATGTTCATGAGTT 162  
QY 68 TTGTGTTGAGAGCAGCAGATGTCACAGTGTATTTAGAGATCACCGCATTTGTTCAG 127  
Db 163 TTGTGTTGAGAGCAGCAGATGTCACAGTGTATTTAGAGATCACCGCATTTGTTCAG 222  
QY 128 CTGCAGAGATGCCGATGGAGTGGAGTTGTACATGAGATTGAGTTCTATGCCAAATGAA 187

Db 223 CTGCAGAGATGCCGATGGAGTGGAGTTGTACATGAGATTGAGTTCTATGCCAAATGAA 282  
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QY 248 GAAGGAAAGGTGCGCTGCGCGCGGCTTACCAAGAGAGATATCAAGCAGTGTGCGTGC 307  
Db 343 GAAGGAAAGGTGCGCTGCGCGCGGCTTACCAAGAGAGATATCAAGCAGTGTGCGTGC 402  
QY 308 TGTGACTTTGATTAACCTGAGAGACTGGGAGAGGGATGAAGAGATGAGCTGCTCATGT 367  
Db 403 TGTGACTTTGATTAACCTGAGAGACTGGGAGAGGGATGAAGAGATGAGCTGCTCATGT 462  
QY 368 GGAACATATGACGACTTTTGAAGAAGTGCAGACCAAGAGACCTCCACCTGCATGGA 427  
Db 463 GGAACATATGACGACTTTTGAAGAAGTGCAGACCAAGAGACCTCCACCTGCATGGA 522

QY 428 TGATTGGAT 437  
Db 523 TGATTGGAT 532

RESULT 6  
AL527833  
LOCUS 934 bp mRNA linear EST 13-FEB-2001  
DEFINITION AL527833.LTI\_NFL003\_NBC3 Homo sapiens cDNA clone CSODC027YD22 5  
prime, mRNA sequence.  
ACCESSION AL527833  
VERSION AL527833.1 GI:12791326  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 934)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
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/clone="CSODC027YD22"  
/clone\_1lb="LTI\_NFL003\_NBC3"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed  
by Life Technologies. Contact : Feng Liang Life  
Technologies, a division of Invitrogen 9800 Medical Center  
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610  
8371 Email : fliang@lifestech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 230 a 209 c 289 g 205 t  
ORIGIN  
Query Match 76.1%; Score 425.2; DB 9; Length 934;  
Best Local Similarity 99.3%; Pred. No. 3.5e-115;  
Matches 427; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GGCACGGCAGCAGCCCGGACCTTGTTGATGACAGAGCCCATGTATGTTCATGAGTT 67  
Db 52 GGGAAAGCAGCAGCCCGGACCTTGTTGATGACAGAGCCCATGTATGTTCATGAGTT 111

QY	68	TTTGTTTGAAGGACACACCAGATGCTCCAGCTGTTATTGAGATCAACCCGATTGTGTGAG	127
Db	112	TTGTGTTAGAGGACACACCGAGTGCACCTGCTTTATTGAGATCAACCCGATTGTGTGAG	171
QY	128	CTGCAGAAATGCCGATGAGATGGAGTTGTACAATGAGATTGAGTTCCAAAGTGA	187
Db	172	CTGCAGAAATGCCGATGAGATGGAGTTGTACAATGAGATTGAGTTCCAAAGTGA	231
QY	188	CTCCAAAGACATCCCAAGGATTAAGCGCTCTTCCCGCTCTATTACTTGTGTTGAGAAATG	247
Db	232	CTCCAAAGACATCCCAAGGATTAAGCGCTCTTCCCGCTCTATTACTTGTGTTGAGAAATG	291
QY	248	GAAGGAAAAGTGGGCGCTGGCCGCGCTTACCAAGGAGGATATCAAGCCCATGTGGCTGTC	307
Db	292	GAAGGAAAAGTGGGCGCTGGCCGCGCTTACCAAGGAGGATATCAAGCCCATGTGGCTGTC	351
QY	308	TGTGACCTTTGATTAAGTGGAGAGACTGGGAAAGGGGATGAAGATGGAAGCTGGCTCATGT	367
Db	352	TGTGACCTTTGATTAAGTGGAGAGACTGGGAAAGGGGATGAAGATGGAAGCTGGCTCATGT	411
QY	368	GGAACATTATGACAGAGCTTTTGAAGAGGTCACGACCAAGAGAGCTCCACCTGGCATGGA	427
Db	412	GGAACATTATGACAGAGCTTTTGAAGAGGTCACGACCAAGAGAGCTCCACCTGGCATGGA	471
QY	428	TGATTGGAT 437	
Db	472	TGATTGGAT 481	

RESULT 7	LOCUS	481 bp	mRNA	linear	EST 25-APR-2001
BF776383	BF776383				
DEFINITION	287175 MRC 3BOV Bos	taurus	CDNA 5'	mRNA sequence.	
ACCESSION	BF776383				

VERSION	BF776383.1	GI:12124283
KEYWORDS	EST.	
SOURCE	COW.	
ORGANISM	Bos taurus	

REFERENCE  
AUTHORS  
Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,  
1 (bases 1 to 481)  
Bovidae, Bovinae, Bos.  
Eumariota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae, Bovinae, Bos.

**TITLE**  
Library evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
genome Res. 11 (4), 626-630 (2001)

**MEDLINE** 21180013  
**COMMENT** Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 333 4370

TEL: 402 762 4388  
Fax: 402 762 4390

Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
Single pass sequencing. Bases called and alt trimmed with nhyred

v0.980904.e. Vector identified by cross\_match with the -mnscore 18 and -mismatch 12 options

and information in options:  
PCR Primers

FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCAGTCACGACG

Plate: 90 row: F column: 22  
Seq primer: ATTTAGGCTGACACTATAG.

FEATURES	Location/Qualifiers
source	1 AR1

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1. 101
/organism="Bos taurus"

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/db_xref="taxon:9913"
/clone_1lb="MARC 3BOV"
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/tissue_type="pooled"
/lab host="DH10B"
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/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

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ORIGIN	BASE COUNT	125 a	98 c	146 g	112 t
Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonsus muscle, and fetal longissimus muscle. "					

Query Match	73.2%;	Score 409;	DB 12;	Length 481;
Best Local Similarity	92.18;	Pred. No. 1.7e-110;		
Matches 443; Conservative	0;	Mismatches 35;	Indels 3;	Gaps

QY 7 TGGACGCGACAGCAGCCCGGACCTTGTGTACGACAGGCCCATGTATGTTTCATGAGT 66  
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Db 1 TGGACGCGACAGCATGCCCGGACCTGTGTGTACGACAGGCCCATGTATGTTTCATGAGT 60

Oy 67 TTGTGTTGGAGACAGCACCAGTCTCACCTGCTTAATTCAGGATCAACCCGATTGTGTTCA 126  
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Db 61 TTTGTCTTGAGACAGCAGCGATGTCACCTGCTCATCGAAGACCAACCGATTGTGTTCA 120

DY 127 GCTCAGAAATGCCGATGGAGTGGAGTTACACATGAGATTGAGTTCTCATGCCAAGTGA 186  
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Dd 121 GCTCCAGAATCTCGATGAGTGAGGTTCACATGAGATTGAGTTCTCATGCCAAGTGA 180

[illegible]

307 CTGCGACCTTGGATTAACCTGGAGAGACAGGGGCAAGGGGCTTGAAGAGATGGAACCTGGCCATAG 365  
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Accession	Sequence	Length
Db	CTGTGGACTTTGATTAACGTGGAGAGACTGGGAAGGGGAAGAAGATGTGGAGCTGGCTCAGG	360
Dy	TGGAACATTATGACAGACCTTTTGAAGAGAGGTTCAGACCAAGAAGAGACCTCCACCTGCCACTGG	426

Y	427	ATGATTTTGGCATGATGATTCGTGACAGTCGTCGATATGTCACAACTAAATTACCTTTCTGTGA	486
Db	361	TGGAGCATTTATGCAGACCTTTGAAAAAGTCTGACACCAAGGAGCACCTCTGCAATGG	420

Db 421 ATGATTGGATGATGATTCTGACAGTGC--CGATGCACACAACTAAATTACCTTCTGTGA 477

D<sub>b</sub> 478 C 478

LOCUS	DEFINITION	EST	IMAGE
B1109957	602901477F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:503125	587 bp	linear
B1109957	602901477F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:503125	587 bp	linear

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
house mouse.  
EST.  
BI109957.1 GI:14560858  
BI109957  
Mamm. sequence.

ORGANISM	REFERENCE
<i>Mus musculus</i>	1 (bases 1 to 587)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	

**AUTHORS** NH-MGC <http://mgc.ncl.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)

Clone distribution by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ELNL at: <http://image.llnl.gov>

FILE: LEAM1106/ ROW: 1 COLUMN: 20

LOCUS	BF308215	824 bp	mRNA	linear	EST 21-NOV-2000
DEFINITION	60188746521 NIH_MGC_17	Homo sapiens	CDNA	clone	IMAGE:4121368 5',
ACCESSION	BF308215	mRNA sequence.			

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VERSION      BF308215.1  GI:11255396
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        NIH-MGC http://mgc.nci.nih.gov/
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Ling Hong/Rubin Laboratory
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
              Plate: LNCM1003 row: a column: 17
              High quality sequence stop: 721.

FEATURES
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    /clone_1lb="NIH_MGC_17"
    /tissue_type="rhabdomyosarcoma"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: muscle; Vector: pOTB7; Site: 1: EcorI;
    Site: 2: XhoI; CDNA made by oligo-dT priming.
    Directionally cloned into EcoRI/XhoI sites using the
    following 5' adaptor: GGCACGAG(G). Size-selected >500bp
    for average insert size 1.8kb. Library constructed by
    Ling Hong in the laboratory of Gerald M. Rubin (University
    of California, Berkeley) using ZAP-CDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
```

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BASE COUNT      210 a      159 c      262 g      193 t
ORIGIN
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Query Match      61.3%; Score 342.8; DB 12; Length 824;
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Best Local Similarity 96.5%; Pred. No. 1e-90;
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Matches 361; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
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QY 1 CCGCAATGCGACGCGACGCGCGACCTTGTGTACGACAGGCCCATGTATGTCTCA 60
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QY 61 TGGAGTTTGTGTGTGAGGACGACCGATGCCAGTCTTATGAGATCACCAGATTG 120
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DB 69 TGGAG-TTTGTGTGTGAGGACGACCGATGCCAGTCTTATGAGATCACCAGATTG 127
QY 121 TGTTCAGCTCAAGATGCCGATGAGTGTGTACATGATGATGATGATGATGATG 180
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DB 128 TGTTCAGCTCAAGATGCCGATGAGTGTGTACATGATGATGATGATGATGATG 187
QY 181 AAGTGAATCCAAAGACTCCCAAGATTAAGCGCTTCCCGCTATTACTTGTGTG 240
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DB 188 AAGTGAATCCAAAGACTCCCAAGATTAAGCGCTTCCCGCTATTACTTGTGTG 247
QY 241 GAAATGAGAGGAAAGAGTGGCTGGCGGGGCTTACCAAGAGAGATCAAGCAATGT 300
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DB 248 GAAATGAGAGGAAAGAGTGGCTGGCGGGGCTTACCAAGAGAGATCAAGCAATGT 307
QY 301 GGGTGTCTGTGACTTTGATTAAGTGTGAGAGACTGTGGAAGGAGATGAGAGTGG 360
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DB 308 GGGTGTCTGTGACTTTGATTAAGTGTGAGAGACTGTGGAAGGAGATGAGAGTGG 367
QY 361 CTCATGTGACAT 374
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DB 368 ATTACAGGACGACAT 381
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RESULT 11

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BG975246
LOCUS       BG975246      635 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION 602843153F1 NCI_CGAP_Mam4 Mus musculus CDNA clone IMAGE:4979028 5',
            mRNA sequence.
ACCESSION   BG975246
VERSION     BG975246.1  GI:14362883
KEYWORDS
SOURCE      EST.
ORGANISM    house mouse.
REFERENCE    Mus musculus
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
COMMENT      NIH-MGC http://mgc.nci.nih.gov/
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: Lotmar Hennighausen Ph.D., Priscilla Furth
              Ph.D.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: LHAM10976 row: 1 column: 13
              High quality sequence stop: 612.

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    /dev_stage="5 months"
    /lab_host="DH10B"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;
    Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
    Library constructed by Life Technologies. Investigators
    providing samples: Lotmar Hennighausen/Priscilla Furth.
    NIH Reference for transgenic model: Li et al., Cell Growth
    and Differentiation 7, 3-11 (1996)."
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ORIGIN
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Best Local Similarity 87.1%; Pred. No. 5.6e-82;
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Matches 378; Conservative 0; Mismatches 53; Indels 3; Gaps 3;
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QY 81 AGACGAGTGTCAAGTCTTATGAGATCAGCGCATGTGTTCAAGTGAAGATGCC 140
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DB 72 AGACGAGTGTCAAGTCTTATGAGATCAGCGCATGTGTTCAAGTGAAGATGCC 131
QY 141 GATGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 200
    |||||||
DB 132 GATGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 191
QY 201 CAGATTAAGCGCTTCCCGCTATTACTTG-TTTGTGGAAGATGAGGAAAGT 259
    |||||||
DB 192 CAGATTAAGCGCTTCCCGCTATTACTTG-TTTGTGGAAGATGAGGAAAGT 251
QY 260 GGCCTGGCCGCG-GCTTACCAAGAGATATCAAGCAGTGTGCTCTGTGACTTTG 318
    |||||||
DB 252 GGCCTGGCCTAGTGTCTCAACAAGAGATATTAAGCCTGTGTGCTCTGTGACTTGG 311
QY 319 ATAACTGGAGAGACTGGGAAGGGGATGA-AGAGATGAGACTGGCTCATGTGAACATTAT 377
    |||||||
DB 312 ATAACTGGAGAGACTGGGAAGGGGATGAAGAGTGTGAGTGTGAGTGTGAACATTAT 371
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QY	378	GCAGAGCTTTGAAACAAGTGAAGCACCAGACAGACTCCACCTGCCATGAGATTTGGAT	437
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QY	438	GATGATTTCTGACAG	451
Db	432	GATGATTTCTGACAG	445
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LOCUS	AK004415		
DEFINITION	AK004415 730 bp mRNA linear HTC 19-JAN-2002		
ACCESSION	AK004415		
VERSION	AK004415.1	GI:12835591	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone:lib.RIKEN full-length enriched mouse cDNA library clone:1110069E20.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, Y., Nishik, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system -384-format		
JOURNAL	sequencing pipeline with 384 multicapillary sequencer		
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	20530913		
REFERENCE			
AUTHORS	4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, O., Fukuda, S., Aikawa, K., Izawa, N., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Koehli, H., Kuell, P., Lewis, S., Matsuo, Y., Nkaido, T., Pesole, G., Quackenbush, J., Schriml, L. M., Stabili, F., Suzuki, R., Tomita, M., Wager, R., Weshio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gaiboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamuya, M., Lee, N. H., Lyons, P., Mochizuki, L., Washima, J., Mazzarelli, J., Nombela, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.		

```

TITLE      Functional annotation of a full-length mouse cDNA collection
JOURNAL    Nature 409 (6821), 685-690 (2001)
MEDLINE    21085660
PUBMED     11217851
REFERENCE  5 (bases 1 to 730)
AUTHORS    Adachi,T., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
           Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bull,C.,
           Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
           Hara,D., Hayatsu,N., Hill,D., Hiramoto,K., Hirooka,T., Horii,F.,
           Hume,D., Imoto,K., Ishii,Y., Itoh,M., Itawa,M., Kasukawa,T.,
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           Saito,H., Saito-R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
           Schirml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
           Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
           Tanaka,T., Tezuka,Y., Toyota,Y., Yamamura,T., Yamanaka,I.,
           Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
           Hayashizaki,Y.

TITLE      Direct Submission
JOURNAL    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
           Physical and Chemical Research (RIKEN), Laboratory for Genome
           Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
           RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
           Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
           URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
           Fax:81-45-503-9216)

COMMENT    Please visit our web site (http://genome.gsc.riken.go.jp/) for
           further details.

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BASE COUNT 172 a 175 c 204 g 179 t
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Query Match 54.7%; Score 305.8; DB 11; Length 730;
Best Local Similarity 84.7%; Pred. No. 9.5e-80;
Matches 343; Conservative 0; Mismatched 62; Indels 0; Gaps 0;
CGCAATGGCAGGCAGCCGCCGACCTTGGAAGACGACGACCAGTATGTATCAT 61
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Db 25 CACCATGGAACGACGACCTGCTGTGTACAGACAGACCAATATGTTTCAT 84  
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 Oy 122 GTTCAGTGCAGAAAGTCCGATGAGTGTGTGATGATGATGATGATGATGATG 181  
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 Oy 182 AGTGAATCCAGAGATCCAGATTAAGCGCTTCCCTCTTATGATGATGATGATG 241  
 Db 205 GGTGATCTCAGAGATCCAGATTAAGCGCTTCCCTCTTATGATGATGATGATG 264  
 Oy 242 AAAATGAGAGAAAGTGGCTGGCGGCTTACCAAGAGATGATGATGATGATG 301  
 Db 265 GAAATGAGAGAAAGTGGCTGGCGGCTTACCAAGAGATGATGATGATGATG 324  
 Oy 302 GCTGTCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 361  
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 Oy 362 TCATGTGGAACATTTATGACAGCTTTTGAAGAAGTCAAGCACCACCA 406  
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RESULT 13  
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 LOCUS  
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700113122:homolog to TELOMERASE-BINDING PROTEIN P23 (HSP90 CO-CHAPERONE) (PROGESTERONE RECEPTOR COMPLEX P23), full insert sequence.  
 AK007198  
 VERSION AK007198.1 GI:12840607  
 KEYWORDS HMC; CAP trapper.  
 SOURCE Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:1700113122.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, N., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20493374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Onoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
 JOURNAL sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS

Alizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Balalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nishida, I., Pesole, R., Quackenbush, J., Schriml, L.M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.D., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Welter, C., Whitlaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851

5 (bases 1 to 1460)  
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Aizawa, T., Balderelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hirotsu, K., Hirotsu, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schiml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shitaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222).  
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

FEATURES  
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Query Match 54.3%; Score 303.6; DB 11; Length 1460;  
 Best Local Similarity 87.2%; Pred. No. 5.9e-79;  
 Matches 333; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2 CGCAATGGCAGCAGCAGCCGACCTTGTGTGACAGACAGCCCATGATGTGTAT 61  
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 DB 766 GGAATTTGT 825  
 QY 122 GTTCAGCTGCAGAGATGCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 181  
 DB 826 GTTCAGCTGCAGAGATGCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 885  
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 QY 242 AAATGTGAG 301  
 DB 946 GAATGTGAG 1005  
 QY 302 GCTGTCTGT 361  
 DB 1006 GCTGTCTGT 1065  
 QY 362 TCATGTGAGACATTTATGAGAG 383  
 DB 1066 TCAGGTGAGACATTTATGAGAG 1087

RESULT 14  
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 LOCUS AL518644 LTI\_NFL011\_NBC1 Homo sapiens CDNA clone CS0DA011YB15 5

DEFINITION prime, mRNA sequence.  
 ACCESSION AL518644  
 VERSION AL518644.1 GI:12782137  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 958)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES  
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 /lab\_host="DH10B"  
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division of Invitrogen 9800 Medical Center Drive Rockville  
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
 fliang@lifestech.com URL :  
 http://fulllength.invitrogen.com"

BASE COUNT 225 a 222 c 295 g 211 t 5 others  
 ORIGIN

Query Match 50.5%; Score 282.4; DB 9; Length 958;  
 Best Local Similarity 97.9%; Pred. No. 9.7e-73;  
 Matches 286; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 8 GGCACGAGCAGACAGCCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 67  
 DB 76 GGCAGAGCAGACAGCCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 135  
 QY 68 TTGT 127  
 DB 136 TTGT 195  
 QY 128 CTGCAAGATGCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 187  
 DB 196 CTGCAAGATGCCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 255  
 QY 188 CTCCAGAGACTCCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247  
 DB 256 CTCCAGAGACTCCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315  
 QY 248 GAGGAG 299  
 DB 316 GAGGAG 367

RESULT 15  
 H32388 325 bp mRNA linear EST 02-APR-1998  
 LOCUS H32388  
 DEFINITION EST107429 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPBV78  
 5' end, mRNA sequence.  
 ACCESSION H32388  
 VERSION H32388.1 GI:977805  
 KEYWORDS EST.  
 SOURCE Rattus sp.  
 ORGANISM Rattus sp.  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 325)  
 AUTHORS Lee, N.H., Weinstein, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fullerton,  
 R.A., Marmaras, S., Glodex, A., Cocayne, J.D., Adams, M.D., Kerlan,  
 A.R., Fraser, C.M. and Venter, J.C.  
 TITLE Comparative expressed-sequence-tag analysis of differential gene  
 expression profiles in PC-12 cells before and after nerve growth  
 factor treatment  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)  
 MEDLINE 95396786  
 COMMENT Contact: Lee, NH  
 The Institute for Genomic Research  
 9712, Medical Center Drive, Rockville, MD 20850, USA  
 Tel: (301)-838-3529  
 Fax: (301)-838-0208  
 Email: nhlee@tigr.org  
 For clone availability please contact the TIGR Database  
 (tdbinfo@tigr.org)  
 Seq primer: M13 Reverse  
 Location/Qualifiers  
 1..325  
 /organism="Rattus sp."  
 /db\_xref="AFCC (Inhost):2002127"  
 /db\_xref="taxon:10118"  
 /clone="RBPV78"  
 /clone\_id="Rat PC-12 cells, untreated"  
 /note="Vector: plasmid SK-; Site: 1; EcoRI; Site: 2; XhoI; poly(A) + RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an

FEATURES  
 source

oligo-dt primer and directionally cloned using the Lambda  
ZAP II Vector Kit by Stratagene"  
BASE COUNT 84 a 71 c 96 g 71 t 3 others  
ORIGIN

Query Match 48.7%; Score 272.4; DB 14; Length 325;  
Best Local Similarity 89.5%; Pred. No. 5.5e-70;  
Matches 291; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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OY 107 GGATCACCAGCATGTGTCAGCTGCAAGATGCCGATGAGTGTGACATGAGAT 166
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Db 1 GGACCACCCGATCGTTCAGCTGCAGAGATGTGATGCTGTGACCTGTACACAGAGAT 60
OY 167 TGAATTATGCAAGTCACTCCAGAGACTCCAGATAAGCGCTTCCCGCTCTAT 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
Db 61 TGANTTCATGCCAANTGAATCCAGAGACTCCAGATAAGCGCTGTGCTCCAT 120
OY 227 TACTGTGTTTGAGAAAATGAGAGAAAAGTGCGCTGCGCGGCTTACCAAGAGGA 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
Db 121 TACTGTGTTTGAGAGAAATGAGAGAGAGTGCGCTGCGCTGCACTCACCAAGAGGA 180
OY 287 TATCAAGCCAGTGTGCTGTCTGTGACTTTGATTAATGAGAGACTGGAGAGGATGA 346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
Db 181 TATAAAGCCCGTTGGCTCTCTGTGACTTCGATAACTGAGAGACTGGAGAGNAGATGA 240
OY 347 AGAGATGAGCTGCTCATGTGGAACATTATCGAGAGCTTTGAAGAAGTCAAGACAA 406
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Db 241 CGAGATGAGAGCTGGCGAGGTGAACACTATGACAGAGCTTTGAACAAAGTCAAGACTAA 300
OY 407 GAGACCTCCACCTGCGCATGATGAT 431
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Db 301 GAGACCTCCCGCTGCCATGATGAT 325
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Search completed: March 20, 2003, 03:50:53  
Job time : 1823 secs